

**In the Claims**

Please amend claims 1 and 7 under the provisions of 37 C.F.R. §1.121(b) by deleting the bracketed material and inserting the underlined material as follows:

--1. (Twice Amended) A system for determining experimentally a plurality of three-dimensional atomic structures, each of which is associated with a corresponding protein, comprising:

a database of sequence information, and known structural information and functional information, which is systematically organized for a plurality of proteins;

at least one bioinformatics tool using the structural information, sequence information and functional information stored in the database to cluster the plurality of proteins into a plurality of families, in which members of each family have corresponding homologous sequences;

protein synthesis means for synthesizing for each family determined by the at least one bioinformatics tool [, in parallel,] a plurality of target proteins, in parallel, which are appropriately representative members of the family, using information stored in the database corresponding to the target proteins, the protein synthesis means having screening means for screening the products of the synthesis to determine ones that are effective as proteins;

protein processing means for preparing, purifying and characterizing each target protein which is determined to be effective by the screening means;

crystallization means for crystallizing each target protein processed by the protein processing means [in parallel] against a plurality of crystallization screens in parallel to produce a plurality of specimen crystals of the target protein, and testing the plurality of specimen crystals for predetermined diffraction characteristics to determine suitable ones of the plurality of specimen crystals of the target protein;

X-ray crystallography means for performing high-throughput crystallography on the specimen crystals of each target protein determined by the crystallization means to be suitable, the X-ray crystallography means having diffraction measuring means for measuring for diffraction data the suitable specimen crystals of the target protein, analyzing means for analyzing the diffraction data, means for building an atomic model of the target protein according to an analysis of the diffraction data by the analyzing means, and means for refining the model of the target protein against the diffraction data and storing the refined model in the database;

structure extraction means having means for analyzing the refined model of the target protein using sequence information corresponding to other family members which is stored in the database and information corresponding to other known three-dimensional structures which is stored in the database, means for analyzing the refined model for functional motifs and for surface characteristics to define active sites and macromolecular contact sites, and means for defining at least one class of compounds predicted to have binding potency using the active sites information corresponding to the target protein; and

a homology model building tool developing a homology model using the refined model of the target protein retrieved from the database,

wherein the database is updated using the at least one bioinformatics tool along with the developed homology model.--

--7. (Twice Amended) A process for determining experimentally a plurality of three-dimensional atomic structures, each of which is associated with a corresponding protein, comprising the steps of:

(a) systematically organizing sequence information, and known structural information and functional information, for a plurality of proteins into a database;

(b) clustering the plurality of proteins into a plurality of families, in which members of each family have corresponding homologous sequences, using at least one bioinformatics tool and the sequence information, structural information and functional information stored in the database;

(c) synthesizing for each family determined in step (b) [, in parallel,] a plurality of target proteins, in parallel, which are appropriately representative members of the family, using information stored in the database corresponding to the plurality of target proteins, and screening products of the synthesis to determine ones that are effective as proteins;

(d) preparing, purifying and characterizing each target protein which is determined to be effective in step (c);

(e) crystallizing each target protein prepared, purified and characterized in step (d) [in parallel] against a plurality of crystallization screens in parallel to produce a plurality of specimen crystals of the target protein;

(f) testing the plurality of specimen crystals of one of the target proteins grown in step (e) for predetermined diffraction characteristics to determine suitable ones of the plurality of specimen crystals of the one target protein;

(g) performing high-throughput crystallography, including measuring for diffraction data the specimen crystals of the one target protein determined in step (f) to be suitable, building an atomic model of the one target protein according to an analysis of the diffraction data, refining the model of the one target protein against the diffraction data, and storing the refined model in the database;

(h) analyzing the refined model, stored in the database in step (g), of the one target protein using sequence information corresponding to other family members which is stored in the database and information corresponding to other known three-dimensional structures which is stored in the database, analyzing the refined model of the one target protein for functional motifs